



#3

SEQUENCE LISTING

<110> P. Croteau, Rodney B.
Bohlmann, Joerg
Steele, Christopher L.
Phillips, Michael A.

<120> Monoterpene Synthases from Grand Fir (Abies Grandis)

<130> WSUR118414

<140> 10/025,145

<141> 2001-12-19

<150> US 09/360,545

<151> 1999-07-26

<150> PCT/US98/14528

<151> 1998-07-10

<150> US 60/052,249

<151> 1997-07-11

<160> 107

<170> PatentIn version 3.1

<210> 1

<211> 2196

<212> DNA

<213> Abies Grandis

<220>

<221> CDS

<222> (69)..(1952)

<223>

<400> 1

tgccggcagc aggttatctt gagcttcctc catataggcc aacacatatc atatcaaagg 60

gagcaaga atg gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc 110

Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys

1

5

10

ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158

Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr

15

20

25

30

aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206

Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr

35

40

45

cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254

Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val

50

55

60

caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302

Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe

65

70

75

ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg 80 85 90	350
gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr 95 100 105 110	398
ctg gat gat gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc Leu Asp Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg 115 120 125	446
ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe 130 135 140	494
aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu 145 150 155	542
gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn 160 165 170	590
tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val 175 180 185 190	638
tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val 195 200 205	686
tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu 210 215 220	734
tat cgg gct tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu 225 230 235	782
gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile 240 245 250	830
cca gtc tcc gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly 255 260 265 270	878
tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr 275 280 285	926
ctt gag aaa gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys 290 295 300	974
ctt tta gaa ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln 305 310 315	1022
caa aag gaa tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg	1070

Gln	Lys	Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	
320						325					330					
cct	aaa	ttg	aca	ttt	gct	cgg	cat	cgt	cat	gtg	gaa	ttc	tac	act	ttg	1118
Pro	Lys	Leu	Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	
335					340					345					350	
gcc	tct	tgt	att	gcc	att	gac	cca	aaa	cat	tct	gca	ttc	aga	cta	ggc	1166
Ala	Ser	Cys	Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	
				355					360					365		
ttc	gcc	aaa	atg	tgt	cat	ctt	gtc	aca	gtt	ttg	gac	gat	att	tac	gac	1214
Phe	Ala	Lys	Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	
			370					375						380		
act	ttt	gga	acg	att	gac	gag	ctt	gaa	ctc	ttc	aca	tct	gca	att	aag	1262
Thr	Phe	Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	
		385					390					395				
aga	tgg	aat	tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	1310
Arg	Trp	Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	
	400					405					410					
gtg	tac	atg	gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	1358
Val	Tyr	Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	
415					420					425					430	
gag	aag	act	caa	ggg	aga	aac	act	ctc	aac	tat	gtt	cga	aag	gct	tgg	1406
Glu	Lys	Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	
				435					440					445		
gag	gct	tat	ttt	gat	tca	tat	atg	gaa	gaa	gca	aaa	tgg	atc	tct	aat	1454
Glu	Ala	Tyr	Phe	Asp	Ser	Tyr	Met	Glu	Glu	Ala	Lys	Trp	Ile	Ser	Asn	
			450					455					460			
ggt	tat	ctg	cca	atg	ttt	gaa	gag	tac	cat	gag	aat	ggg	aaa	gtg	agc	1502
Gly	Tyr	Leu	Pro	Met	Phe	Glu	Glu	Tyr	His	Glu	Asn	Gly	Lys	Val	Ser	
		465					470					475				
tct	gca	tat	cgc	gta	gca	aca	ttg	caa	ccc	atc	ctc	act	ttg	aat	gca	1550
Ser	Ala	Tyr	Arg	Val	Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asn	Ala	
	480					485					490					
tgg	ctt	cct	gat	tac	atc	ttg	aag	gga	att	gat	ttt	cca	tcc	agg	ttc	1598
Trp	Leu	Pro	Asp	Tyr	Ile	Leu	Lys	Gly	Ile	Asp	Phe	Pro	Ser	Arg	Phe	
495					500					505					510	
aat	gat	ttg	gca	tcg	tcc	ttc	ctt	cgg	cta	cga	ggt	gac	aca	cgc	tgc	1646
Asn	Asp	Leu	Ala	Ser	Ser	Phe	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	
				515					520					525		
tac	aag	gcc	gat	agg	gat	cgt	ggt	gaa	gaa	gct	tcg	tgt	ata	tca	tgt	1694
Tyr	Lys	Ala	Asp	Arg	Asp	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	Cys	
			530					535					540			
tat	atg	aaa	gac	aat	cct	gga	tca	acc	gaa	gaa	gat	gcc	ctc	aat	cat	1742
Tyr	Met	Lys	Asp	Asn	Pro	Gly	Ser	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	
		545					550					555				
atc	aat	gcc	atg	gtc	aat	gac	ata	atc	aaa	gaa	tta	aat	tgg	gaa	ctt	1790
Ile	Asn	Ala	Met	Val	Asn	Asp	Ile	Ile	Lys	Glu	Leu	Asn	Trp	Glu	Leu	

560	565	570	
cta aga tcc aac gac aat att cca atg ctg gcc aag aaa cat gct ttt			1838
Leu Arg Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe			
575	580	585	590
gac ata aca aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt			1886
Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe			
	595	600	605
agt gtt gcc aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt			1934
Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu			
	610	615	620
gaa tct atg ctt ttt taa ctataacccat atccataata ataagctcat			1982
Glu Ser Met Leu Phe			
	625		
aatgctaaat tattggcctt atgacatagt ttatgtatgt acttgtgtga attcaatcat			2042
atcgtgtggg tatgattaaa aagctagagc ttactagggt agtaacatgg tgataaaaagt			2102
tataaaatgt gagttataga gatacccatg ttgaataatg aattacaaaa agagaaattt			2162
atgtagaata agattggaag cttttcaatt gttt			2196
<210> 2			
<211> 627			
<212> PRT			
<213> Abies Grandis			
<400> 2			
Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg			
1	5	10	15
Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr			
	20	25	30
Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser			
	35	40	45
Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg			
	50	55	60
Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln			
65	70	75	80
Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu			
	85	90	95
Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp			
	100	105	110

Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
130 135 140

Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
145 150 155 160

Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
165 170 175

Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
210 215 220

Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
225 230 235 240

Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270

Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
355 360 365

Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
405 410 415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
420 425 430

Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
435 440 445

Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
450 455 460

Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
465 470 475 480

Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
515 520 525

Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
530 535 540

Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
545 550 555 560

Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
565 570 575

Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val

Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
 610 615 620

Met Leu Phe.
 625

<210> 3
 <211> 2018
 <212> DNA
 <213> Abies Grandis

<220>
 <221> CDS
 <222> (6)..(1892)
 <223>

<400> 3
 cagca atg gct cta gtt tct acc gca ccg ttg gct tcc aaa tca tgc ctg 50
 Met Ala Leu Val Ser Thr Ala Pro Leu Ala Ser Lys Ser Cys Leu
 1 5 10 15

cac aaa tcg ttg atc agt tct acc cat gag ctt aag gct ctc tct aga 98
 His Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg
 20 25 30

aca att cca gct cta gga atg agt agg cga ggg aaa tct atc act cct 146
 Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro
 35 40 45

tcc atc agc atg agc tct acc acc gtt gta acc gat gat ggt gta cga 194
 Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg
 50 55 60

aga cgc atg ggc gat ttc cat tcc aac ctc tgg gac gat gat gtc ata 242
 Arg Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile
 65 70 75

cag tct tta cca acg gct tat gag gaa aaa tcg tac ctg gag cgt gct 290
 Gln Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala
 80 85 90 95

gag aaa ctg atc ggg gaa gta aag aac atg ttc aat tcg atg tca tta 338
 Glu Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu
 100 105 110

gaa gat gga gag tta atg agt ccg ctc aat gat ctc att caa cgc ctt 386
 Glu Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu
 115 120 125

tgg att gtc gac agc ctt gaa cgt ttg ggg atc cat aga cat ttc aaa 434
 Trp Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys
 130 135 140

gat gag ata aaa tcg gcg ctt gat tat gtt tac agt tat tgg ggc gaa 482
 Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu

145	150	155	
aat ggc atc gga tgc ggg agg gag agt gtt gtt act gat ctg aac tca Asn Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser 160 165 170 175			530
act gcg ttg ggg ctt cga acc cta cga cta cac gga tac ccg gtg tct Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Pro Val Ser 180 185 190			578
tca gat gtt ttc aaa gct ttc aaa ggc caa aat ggg cag ttt tcc tgc Ser Asp Val Phe Lys Ala Phe Lys Gly Gln Asn Gly Gln Phe Ser Cys 195 200 205			626
tct gaa aat att cag aca gat gaa gag atc aga ggc gtt ctg aat tta Ser Glu Asn Ile Gln Thr Asp Glu Glu Ile Arg Gly Val Leu Asn Leu 210 215 220			674
ttc cgg gcc tcc ctc att gcc ttt cca ggg gag aaa att atg gat gag Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Ile Met Asp Glu 225 230 235			722
gct gaa atc ttc tct acc aaa tat tta aaa gaa gcc ctg caa aag att Ala Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu Ala Leu Gln Lys Ile 240 245 250 255			770
ccg gtc tcc agt ctt tcg cga gag atc ggg gac gtt ttg gaa tat ggt Pro Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly 260 265 270			818
tgg cac aca tat ttg ccg cga ttg gaa gca agg aat tac atc caa gtc Trp His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Gln Val 275 280 285			866
ttt gga cag gac act gag aac acg aag tca tat gtg aag agc aaa aaa Phe Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr Val Lys Ser Lys Lys 290 295 300			914
ctt tta gaa ctc gca aaa ttg gag ttc aac atc ttt caa tcc tta caa Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Gln Ser Leu Gln 305 310 315			962
aag agg gag tta gaa agt ctg gtc aga tgg tgg aaa gaa tcg ggt ttt Lys Arg Glu Leu Glu Ser Leu Val Arg Trp Trp Lys Glu Ser Gly Phe 320 325 330 335			1010
cct gag atg acc ttc tgc cga cat cgt cac gtg gaa tac tac act ttg Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu 340 345 350			1058
gct tcc tgc att gcg ttc gag cct caa cat tct gga ttc aga ctc ggc Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly 355 360 365			1106
ttt gcc aag acg tgt cat ctt atc acg gtt ctt gac gat atg tac gac Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp 370 375 380			1154
acc ttc ggc aca gta gac gag ctg gaa ctc ttc aca gcg aca atg aag Thr Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Met Lys 385 390 395			1202

aga tgg gat ccg tcc tcg ata gat tgc ctt cca gaa tat atg aaa gga	1250
Arg Trp Asp Pro Ser Ser Ile Asp Cys Leu Pro Glu Tyr Met Lys Gly	
400 405 410 415	
gtg tac ata gcg gtt tac gac acc gta aat gaa atg gct cga gag gca	1298
Val Tyr Ile Ala Val Tyr Asp Thr Val Asn Glu Met Ala Arg Glu Ala	
420 425 430	
gag gag gct caa ggc cga gat acg ctc aca tat gct cgg gaa gct tgg	1346
Glu Glu Ala Gln Gly Arg Asp Thr Leu Thr Tyr Ala Arg Glu Ala Trp	
435 440 445	
gag gct tat att gat tcg tat atg caa gaa gca agg tgg atc gcc act	1394
Glu Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala Arg Trp Ile Ala Thr	
450 455 460	
ggt tac ctg ccc tcc ttt gat gag tac tac gag aat ggg aaa gtt agc	1442
Gly Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu Asn Gly Lys Val Ser	
465 470 475	
tgt ggt cat cgc ata tcc gca ttg caa ccc att ctg aca atg gac atc	1490
Cys Gly His Arg Ile Ser Ala Leu Gln Pro Ile Leu Thr Met Asp Ile	
480 485 490 495	
ccc ttt cct gat cat atc ctc aag gaa gtt gac ttc cca tca aag ctt	1538
Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu	
500 505 510	
aac gac ttg gca tgt gcc atc ctt cga tta cga ggt gat acg cgg tgc	1586
Asn Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys	
515 520 525	
tac aag gcg gac agg gct cgt gga gaa gaa gct tcc tct ata tca tgt	1634
Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys	
530 535 540	
tat atg aaa gac aat cct gga gta tca gag gaa gat gct ctc gat cat	1682
Tyr Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His	
545 550 555	
atc aac gcc atg atc agt gac gta atc aaa gga tta aat tgg gaa ctt	1730
Ile Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu	
560 565 570 575	
ctc aaa cca gac atc aat gtt ccc atc tcg gcg aag aaa cat gct ttt	1778
Leu Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe	
580 585 590	
gac atc gcc aga gct ttc cat tac ggc tac aaa tac cga gac ggc tac	1826
Asp Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr	
595 600 605	
agc gtt gcc aac gtt gaa acg aag agt ttg gtc acg aga acc ctc ctt	1874
Ser Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu	
610 615 620	
gaa tct gtg cct ttg tag caacagctca aatctatgcc ctatgctatg	1922
Glu Ser Val Pro Leu	
625	

tcgggttaaa atatatgtgg aaggtagccg ttggatgtag aggataagtt tgttataatt 1982

taataaagtt gtaatttaaa aaaaaaaaaa aaaaaa 2018

<210> 4
<211> 628
<212> PRT
<213> Abies Grandis

<400> 4

Met Ala Leu Val Ser Thr Ala Pro Leu Ala Ser Lys Ser Cys Leu His
1 5 10 15

Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg Thr
20 25 30

Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro Ser
35 40 45

Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg Arg
50 55 60

Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile Gln
65 70 75 80

Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala Glu
85 90 95

Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu Glu
100 105 110

Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu Trp
115 120 125

Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys Asp
130 135 140

Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu Asn
145 150 155 160

Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser Thr
165 170 175

Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Pro Val Ser Ser
180 185 190

Asp Val Phe Lys Ala Phe Lys Gly Gln Asn Gly Gln Phe Ser Cys Ser

195

200

205

Glu Asn Ile Gln Thr Asp Glu Glu Ile Arg Gly Val Leu Asn Leu Phe
 210 215 220

Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Ile Met Asp Glu Ala
 225 230 235 240

Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro
 245 250 255

Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly Trp
 260 265 270

His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Gln Val Phe
 275 280 285

Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr Val Lys Ser Lys Lys Leu
 290 295 300

Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Gln Ser Leu Gln Lys
 305 310 315 320

Arg Glu Leu Glu Ser Leu Val Arg Trp Trp Lys Glu Ser Gly Phe Pro
 325 330 335

Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu Ala
 340 345 350

Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly Phe
 355 360 365

Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Thr
 370 375 380

Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Met Lys Arg
 385 390 395 400

Trp Asp Pro Ser Ser Ile Asp Cys Leu Pro Glu Tyr Met Lys Gly Val
 405 410 415

Tyr Ile Ala Val Tyr Asp Thr Val Asn Glu Met Ala Arg Glu Ala Glu
 420 425 430

Glu Ala Gln Gly Arg Asp Thr Leu Thr Tyr Ala Arg Glu Ala Trp Glu
 435 440 445

Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala Arg Trp Ile Ala Thr Gly
450 455 460

Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu Asn Gly Lys Val Ser Cys
465 470 475 480

Gly His Arg Ile Ser Ala Leu Gln Pro Ile Leu Thr Met Asp Ile Pro
485 490 495

Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
500 505 510

Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
515 520 525

Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
530 535 540

Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
545 550 555 560

Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu
565 570 575

Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr Ser
595 600 605

Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu Glu
610 615 620

Ser Val Pro Leu
625

<210> 5
<211> 2089
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (73)..(1986)
<223>

<400> 5
tgccgttttaa tcggttttaa gaagctacca tagttcgggt taaagaagct accatagttt 60
aggcaggaat cc atg gct ctc ctt tct atc gta tct ttg cag gtt ccc aaa 111
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys
1 5 10
tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala
15 20 25
ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
30 35 40 45
aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp
50 55 60
gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303
Asp Asn Gly Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
65 70 75
aac ctg tgg gaa gat gat ttc ata caa tca ttg tcc tca cct tat ggg 351
Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly
80 85 90
gga tct tcg tac agt gaa cgt gct gag aca gtc gtt gag gaa gta aaa 399
Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Glu Glu Val Lys
95 100 105
gag atg ttc aat tca ata cca aat aat aga gaa tta ttt ggt tcc caa 447
Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln
110 115 120 125
aat gat ctc ctt aca cgc ctt tgg atg gtg gat agc att gaa cgt ctg 495
Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu
130 135 140
ggg ata gat aga cat ttc caa aat gag ata aga gta gcc ctc gat tat 543
Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr
145 150 155
gtt tac agt tat tgg aag gaa aag gaa ggc att ggg tgt ggc aga gat 591
Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp
160 165 170
tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt 639
Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu
175 180 185
cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa 687
Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys
190 195 200 205
gat gaa aag ggg cat ttt gcc tgc cct gca atc cta acc gag gga cag 735
Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln
210 215 220
atc act aga agt gtt cta aat tta tat cgg gct tcc ctg gtc gcc ttt 783
Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe

225	230	235	
ccc ggg gag aaa gtt atg gaa gag gct gaa atc ttc tgc gca tct tat Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr 240 245 250			831
ttg aaa aaa gtc tta caa aag att ccg gtc tcc aat ctt tca gga gag Leu Lys Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu 255 260 265			879
ata gaa tat gtt ttg gaa tat ggt tgg cac acg aat ttg ccg aga ttg Ile Glu Tyr Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu 270 275 280 285			927
gaa gca aga aat tat atc gag gtc tac gag cag agc ggc tat gaa agc Glu Ala Arg Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser 290 295 300			975
tta aac gag atg cca tat atg aac atg aag aag ctt tta caa ctt gca Leu Asn Glu Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala 305 310 315			1023
aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln 320 325 330			1071
tct atc tcc aga tgg tgg aaa gaa tca ggt tgc tct caa ctg act ttt Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe 335 340 345			1119
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser 350 355 360 365			1167
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys 370 375 380			1215
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met 385 390 395			1263
aac gaa ctc caa ctt ttt acg gat gca att aag aga tgg gat ttg tca Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser 400 405 410			1311
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu 415 420 425			1359
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly 430 435 440 445			1407
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp 450 455 460			1455
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr 465 470 475			1503

ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata 1551
Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile
480 485 490

gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac 1599
Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr
495 500 505

ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg 1647
Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser
510 515 520 525

tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg 1695
Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg
530 535 540

gcc cgt gga gaa gaa gct tca gct ata tcg tgt tat atg aaa gac cat 1743
Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His
545 550 555

cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc 1791
Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile
560 565 570

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc 1839
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser
575 580 585

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct 1887
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala
590 595 600 605

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac 1935
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn
610 615 620

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg 1983
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

taa aaacatatag aatgcattaa aatgtgggaa gtctataatc tagactattc 2036

tctatctttc ataatgtaga tctggatgtg tattgaactc taataaaaaaa aaa 2089

<210> 6
<211> 637
<212> PRT
<213> Abies Grandis

<400> 6

Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
1 5 10 15

Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys
245 250 255

Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr
260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg

275

280

285

Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu
 290 295 300

Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu
 305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser
 325 330 335

Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His
 340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro
 355 360 365

Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val
 370 375 380

Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu
 385 390 395 400

Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg
 405 410 415

Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys
 420 425 430

Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly Arg Asp Met
 435 440 445

Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met
 450 455 460

Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr Phe Glu Glu
 465 470 475 480

Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu
 485 490 495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln
 500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu
 515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser
545 550 555 560

Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PCR primer A

<220>
<221> misc_feature
<222> (1)..(25)
<223> Wherein N=inosine

<400> 7
arraygarra nggnrartay aarga

25

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PCR primer B

<220>
<221> misc_feature
<222> (1)..(20)
<223> Wherein N=inosine residue

<400> 8		
atgytn Cary tntaygargc		20
<210> 9		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Degenerate oligonucleotide PCR primer C		
<220>		
<221> misc_feature		
<222> (1)..(24)		
<223> Wherein N=inosine residue		
<400> 9		
ctnkynrang gncratrta ckty		24
<210> 10		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Degenerate oligonucleotide PCR primer D		
<220>		
<221> misc_feature		
<222> (1)..(23)		
<223> Wherein N=isonine		
<400> 10		
gaygaynnnt wygaygcnya ygg		23
<210> 11		
<211> 108		
<212> DNA		
<213> Abies Grandis		
<400> 11		
gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg		60
agaagatggg acctctcctt tacagacaac ttccccgatt acatgaaa		108
<210> 12		
<211> 104		
<212> DNA		
<213> Abies Grandis		
<400> 12		
gacgacgggt atgatgcgca tggaacgatt gacgagcttg aactcttcac atctgcaatt		60
aagagatgga attcatcaga gatagacagc ttccccgact atat		104

<210> 13
<211> 105
<212> DNA
<213> Abies Grandis

<220>
<221> misc_feature
<222> (1)..(105)
<223> Wherein N=A, C, G or T

<400> 13
gatgatgggt atgatgcgta cggaacgttg gaagaaatca aaatcatgac agaggggagtg 60
agacgatggg atctttcggt gaccgcttnc cccgactata tgaaa 105

<210> 14
<211> 117
<212> DNA
<213> Abies Grandis

<220>
<221> misc_feature
<222> (1)..(117)
<223> Wherein N=A, C, G or T

<400> 14
gacgatgggt atgatgcgca tggaaccttg gaccaactca aaatctttac agaggggagtg 60
agacgatggg atgtttcggt ggtagaccac ttncctccgac tacatgcaat ctagacc 117

<210> 15
<211> 2424
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (2)..(2350)
<223>

<400> 15
g ggt tat gat ctt gtg cat tct ctt aaa tca cct tat att gat tct agt 49
Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser
1 5 10 15

tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97
Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

aat cca gct att aca gga gat gga gaa tca atg att act cca tct gct 145
Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala
35 40 45

tat gac aca gca tgg gta gcg agg gtg ccc gcc att gat ggc tct gct 193

Tyr	Asp	Thr	Ala	Trp	Val	Ala	Arg	Val	Pro	Ala	Ile	Asp	Gly	Ser	Ala		
50						55					60						
cgc	ccg	caa	ttt	ccc	caa	aca	gtt	gac	tgg	att	ttg	aaa	aac	cag	tta	241	
Arg	Pro	Gln	Phe	Pro	Gln	Thr	Val	Asp	Trp	Ile	Leu	Lys	Asn	Gln	Leu		
65					70					75					80		
aaa	gat	ggg	tca	tgg	gga	att	cag	tcc	cac	ttt	ctg	ctg	tcc	gac	cgt	289	
Lys	Asp	Gly	Ser	Trp	Gly	Ile	Gln	Ser	His	Phe	Leu	Leu	Ser	Asp	Arg		
				85					90					95			
ctt	ctt	gcc	act	ctt	tct	tgt	gtt	ctt	gtg	ctc	ctt	aaa	tgg	aac	gtt	337	
Leu	Leu	Ala	Thr	Leu	Ser	Cys	Val	Leu	Val	Leu	Leu	Lys	Trp	Asn	Val		
			100					105						110			
ggg	gat	ctg	caa	gta	gag	cag	gga	att	gaa	ttc	ata	aag	agc	aat	ctg	385	
Gly	Asp	Leu	Gln	Val	Glu	Gln	Gly	Ile	Glu	Phe	Ile	Lys	Ser	Asn	Leu		
		115					120					125					
gaa	cta	gta	aag	gat	gaa	acc	gat	caa	gat	agc	ttg	gta	aca	gac	ttt	433	
Glu	Leu	Val	Lys	Asp	Glu	Thr	Asp	Gln	Asp	Ser	Leu	Val	Thr	Asp	Phe		
		130					135				140						
gag	atc	ata	ttt	cct	tct	ctg	tta	aga	gaa	gct	caa	tct	ctg	cgc	ctc	481	
Glu	Ile	Ile	Phe	Pro	Ser	Leu	Leu	Arg	Glu	Ala	Gln	Ser	Leu	Arg	Leu		
145					150					155					160		
gga	ctt	ccc	tac	gac	ctg	cct	tat	ata	cat	ctg	ttg	cag	act	aaa	cgg	529	
Gly	Leu	Pro	Tyr	Asp	Leu	Pro	Tyr	Ile	His	Leu	Leu	Gln	Thr	Lys	Arg		
				165					170					175			
cag	gaa	aga	tta	gca	aaa	ctt	tca	agg	gag	gaa	att	tat	gcg	gtt	ccg	577	
Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Arg	Glu	Glu	Ile	Tyr	Ala	Val	Pro		
			180					185					190				
tcg	cca	ttg	ttg	tat	tct	tta	gag	gga	ata	caa	gat	ata	ggt	gaa	tgg	625	
Ser	Pro	Leu	Leu	Tyr	Ser	Leu	Glu	Gly	Ile	Gln	Asp	Ile	Val	Glu	Trp		
		195					200					205					
gaa	cga	ata	atg	gaa	gtt	caa	agt	cag	gat	ggg	tct	ttc	tta	agc	tca	673	
Glu	Arg	Ile	Met	Glu	Val	Gln	Ser	Gln	Asp	Gly	Ser	Phe	Leu	Ser	Ser		
		210				215					220						
cct	gct	tct	act	gcc	tgc	gtt	ttc	atg	cac	aca	gga	gac	gcg	aaa	tgc	721	
Pro	Ala	Ser	Thr	Ala	Cys	Val	Phe	Met	His	Thr	Gly	Asp	Ala	Lys	Cys		
225					230					235					240		
ctt	gaa	ttc	ttg	aac	agt	gtg	atg	atc	aag	ttt	gga	aat	ttt	gtt	ccc	769	
Leu	Glu	Phe	Leu	Asn	Ser	Val	Met	Ile	Lys	Phe	Gly	Asn	Phe	Val	Pro		
				245					250					255			
tgc	ctg	tat	cct	gtg	gat	ctg	ctg	gaa	cgc	ctg	ttg	atc	gta	gat	aat	817	
Cys	Leu	Tyr	Pro	Val	Asp	Leu	Leu	Glu	Arg	Leu	Leu	Ile	Val	Asp	Asn		
			260					265					270				
att	gta	cgc	ctt	gga	atc	tat	aga	cac	ttt	gaa	aag	gaa	atc	aag	gaa	865	
Ile	Val	Arg	Leu	Gly	Ile	Tyr	Arg	His	Phe	Glu	Lys	Glu	Ile	Lys	Glu		
		275					280					285					
gct	ctt	gat	tat	gtt	tac	agg	cat	tgg	aac	gaa	aga	gga	att	ggg	tgg	913	
Ala	Leu	Asp	Tyr	Val	Tyr	Arg	His	Trp	Asn	Glu	Arg	Gly	Ile	Gly	Trp		

290	295	300	
ggc aga cta aat ccc ata gca gat ctt gag acc act gct ttg gga ttt			961
Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe			
305	310	315	320
cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac			1009
Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp			
	325	330	335
aac ttc aaa gat gcc aat ggg aaa ttc att tgc tgc acc ggt caa ttc			1057
Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe			
	340	345	350
aac aaa gat gta gca agc atg ctg aat ctt tat aga gct tcc cag ctc			1105
Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu			
	355	360	365
gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act			1153
Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr			
	370	375	380
aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg			1201
Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp			
	385	390	400
aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act			1249
Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr			
	405	410	415
tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa			1297
Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln			
	420	425	430
gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta			1345
Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu			
	435	440	445
ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc			1393
Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe			
	450	455	460
aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc			1441
Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser			
	465	470	475
480			
tgg ttt aga gat tgc ggg ttg cca cta ttc acc ttc gct cgg gag agg			1489
Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg			
	485	490	495
ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag			1537
Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln			
	500	505	510
tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act			1585
Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr			
	515	520	525
gtt ctg gac gat atg tat gac act tat gga acc cta gat gaa ttg aag			1633
Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys			
	530	535	540

cta ttc act gag gct gtg aga aga tgg gac ctc tcc ttt aca gaa aac	1681
Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn	
545 550 555 560	
ctt cca gac tat atg aaa cta tgt tac caa atc tat tat gac ata gtt	1729
Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val	
565 570 575	
cac gag gtg gct tgg gag gca gag aag gaa cag ggg cgt gaa ttg gtc	1777
His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val	
580 585 590	
agc ttt ttc aga aag gga tgg gag gat tat ctt ctg ggt tat tat gaa	1825
Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu	
595 600 605	
gaa gct gaa tgg tta gct gct gag tat gtg cct acc ttg gac gag tac	1873
Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr	
610 615 620	
ata aag aat gga atc aca tct atc ggc caa cgt ata ctt ctg ttg agt	1921
Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser	
625 630 635 640	
gga gtg ttg ata atg gat ggg caa ctc ctt tcg caa gag gca tta gag	1969
Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu	
645 650 655	
aaa gta gat tat cca gga aga cgt gtt ctc aca gag ctg aat agc ctc	2017
Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu	
660 665 670	
att tcc cgc ctg gcg gat gac acg aag aca tat aaa gct gag aag gct	2065
Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala	
675 680 685	
cgt gga gaa ttg gcg tcc agc att gaa tgt tac atg aaa gac cat cct	2113
Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro	
690 695 700	
gaa tgt aca gag gaa gag gct ctc gat cac atc tat agc att ctg gag	2161
Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu	
705 710 715 720	
ccg gcg gtg aag gaa ctg aca aga gag ttt ctg aag ccc gac gac gtc	2209
Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val	
725 730 735	
cca ttc gcc tgc aag aag atg ctt ttc gag gag aca aga gtg acg atg	2257
Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met	
740 745 750	
gtg ata ttc aag gat gga gat gga ttc ggt gtt tcc aaa tta gaa gtc	2305
Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val	
755 760 765	
aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa	2350
Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu	
770 775 780	

tcaaaatagt tgcaataata attgaaataa tgtcaactat gtttcacaaa aaaaaaaaaa 2410
aaaaaaaaaa aaaa 2424

<210> 16
<211> 782
<212> PRT
<213> Abies Grandis

<400> 16

Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser
1 5 10 15

Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala
35 40 45

Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
50 55 60

Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
65 70 75 80

Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
85 90 95

Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val
100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
115 120 125

Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
130 135 140

Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
145 150 155 160

Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp

195

200

205

Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
210 215 220

Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
225 230 235 240

Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro
245 250 255

Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn
260 265 270

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu
275 280 285

Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp
290 295 300

Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe
305 310 315 320

Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp
325 330 335

Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe
340 345 350

Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu
355 360 365

Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr
370 375 380

Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
385 390 395 400

Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr
405 410 415

Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
420 425 430

Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu
435 440 445

Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe
450 455 460

Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser
465 470 475 480

Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg
485 490 495

Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln
500 505 510

Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr
515 520 525

Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys
530 535 540

Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn
545 550 555 560

Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val
565 570 575

His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val
580 585 590

Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu
595 600 605

Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr
610 615 620

Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser
625 630 635 640

Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu
645 650 655

Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu
660 665 670

Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala
675 680 685

Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro
690 695 700

Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu
705 710 715 720

Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val
725 730 735

Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met
740 745 750

Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val
755 760 765

Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
770 775 780

<210> 17
<211> 1967
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (3)..(1736)
<223>

<400> 17
tt tct gaa tct tcc atc cct cga cgc aca ggg aat cat cac gga aat 47
Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His His Gly Asn
1 5 10 15

gtg tgg gac gat gac ctc ata cac tct ctc aac tcg ccc tat ggg gca 95
Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala
20 25 30

cct gca tat tat gag ctc ctt caa aag ctt att gag gag atc aag cat 143
Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His
35 40 45

tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat gat tta atc 191
Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile
50 55 60

aaa cgt ctt cag atc gtt gac act ttg gaa tgc ctg gga atc gat aga 239
Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg
65 70 75

cat ttt gaa cac gaa ata caa aca gct gct tta gat tac gtt tac aga 287
His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg
80 85 90 95

tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat tcc ttc agc	335
Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser	
100 105 110	
aaa gat ctc aac gct aca gct tta gga ttt cgc gct ctc cga ctg cat	383
Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His	
115 120 125	
cga tat aac gta tgc tca ggt gtg ttg aag aat ttc aag gat gaa aac	431
Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn	
130 135 140	
ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga gga gat aaa	479
Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys	
145 150 155	
caa gtg aga agc atg ttg tgc tta ctt cga gct tca gag att tgc ttt	527
Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe	
160 165 170 175	
ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca aga gaa tat	575
Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr	
180 185 190	
cta aac caa gtt tta gct gga cac ggg gat gtg act gac gtg gat caa	623
Leu Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln	
195 200 205	
agc ctt ttg gag aga ggt gaa gta cgc att gga gtt tcc atg gct tgc	671
Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys	
210 215 220	
agt gtg ccg aga tgg gag gca agg agc ttt ctc gaa ata tat gga cac	719
Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His	
225 230 235	
aac cat tgc tgg ctc aag tgc aat atc aac caa aaa atg ttg aag tta	767
Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu	
240 245 250 255	
gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac aag gag ata	815
Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile	
260 265 270	
cag ttt att aca agg tgg tgg aga gac tgc ggt ata tgc cag ctg aat	863
Gln Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn	
275 280 285	
ttc tat cga aag cga cac gtg gaa tat tat tct tgg gtt gtt atg tgc	911
Phe Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys	
290 295 300	
att ttt gag cca gag ttc tct gaa agt aga att gcc ttc gcc aaa act	959
Ile Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr	
305 310 315	
gct atc cta tgt act gtt cta gat gac ctc tat gat acg cac gca acg	1007
Ala Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr	
320 325 330 335	
ttg cat gaa atc aaa atc atg aca gag gga gtg aga cga tgg gat ctt	1055

Leu His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu	
340 345 350	
tcg ttg aca gat gac ctc cca gac tac att aaa att gca ttc cag ttc	1103
Ser Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe	
355 360 365	
ttc ttc aat aca gtg aat gaa ttg ata gtt gaa atc gtg aaa cgg caa	1151
Phe Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln	
370 375 380	
ggg cgg gat atg aca acc ata gtt aaa gat tgc tgg aag cga tac att	1199
Gly Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile	
385 390 395	
gag tct tat ctg caa gaa gcg gaa tgg ata gca act gga cat att ccc	1247
Glu Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro	
400 405 410 415	
act ttt aac gaa tac ata aag aac ggc atg gct agc tca ggg atg tgt	1295
Thr Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys	
420 425 430	
att gta aat ttg aat cca ctt ctc ttg ttg ggt aaa ctt ctc ccc gac	1343
Ile Val Asn Leu Asn Pro Leu Leu Leu Leu Gly Lys Leu Leu Pro Asp	
435 440 445	
aac att ctg gag caa ata cat tct cca tcc aag atc ctg gac ctc tta	1391
Asn Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu	
450 455 460	
gaa ttg acg ggc aga atc gcc gat gac tta aaa gat ttc gag gac gag	1439
Glu Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu	
465 470 475	
aag gaa cgc ggg gag atg gct tca tct tta cag tgt tat atg aaa gaa	1487
Lys Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu	
480 485 490 495	
aat cct gaa tct aca gtg gaa aat gct tta aat cac ata aaa ggc atc	1535
Asn Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile	
500 505 510	
ctt aat cgt tcc ctt gag gaa ttt aat tgg gag ttt atg aag cag gat	1583
Leu Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp	
515 520 525	
agt gtc cca atg tgt tgc aag aaa ttc act ttc aat ata ggt cga gga	1631
Ser Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly	
530 535 540	
ctt caa ttc atc tac aaa tac aga gac ggc tta tac att tct gac aag	1679
Leu Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys	
545 550 555	
gaa gta aag gac cag ata ttc aaa att cta gtc cac caa gtt cca atg	1727
Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met	
560 565 570 575	
gag gaa tag tgatggtctt gggtgtagtt gtctattatg gtatattgca	1776
Glu Glu	

ttgacattta tgcttaaagg tgtttcttaa acgtttaggg cggaccggtta aataagttgg 1836
 caataattaa tatttagaga ctttgtggaa gtgttttaggg cataaaattg cctatggcct 1896
 atggcaagct acaaattgaa attgttgtgt ttataatatt tttattttat ttaaaaaaaaa 1956
 aaaaaaaaa a 1967

<210> 18
 <211> 577
 <212> PRT
 <213> Abies Grandis

<400> 18

Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His His Gly Asn Val
 1 5 10 15

Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala Pro
 20 25 30

Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His Leu
 35 40 45

Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile Lys
 50 55 60

Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg His
 65 70 75 80

Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg Trp
 85 90 95

Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser Lys
 100 105 110

Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg
 115 120 125

Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly
 130 135 140

Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln
 145 150 155 160

Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe Pro
 165 170 175

Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr Leu
180 185 190

Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln Ser
195 200 205

Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys Ser
210 215 220

Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His Asn
225 230 235 240

His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu Ala
245 250 255

Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile Gln
260 265 270

Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn Phe
275 280 285

Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys Ile
290 295 300

Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr Ala
305 310 315 320

Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr Leu
325 330 335

His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu Ser
340 345 350

Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe Phe
355 360 365

Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln Gly
370 375 380

Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile Glu
385 390 395 400

Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro Thr
405 410 415

Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys Ile
 420 425 430

Val Asn Leu Asn Pro Leu Leu Leu Leu Gly Lys Leu Leu Pro Asp Asn
 435 440 445

Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu Glu
 450 455 460

Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu Lys
 465 470 475 480

Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu Asn
 485 490 495

Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile Leu
 500 505 510

Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp Ser
 515 520 525

Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly Leu
 530 535 540

Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys Glu
 545 550 555 560

Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met Glu
 565 570 575

Glu

<210> 19
 <211> 1416
 <212> DNA
 <213> Abies Grandis

<220>
 <221> CDS
 <222> (3)..(1199)
 <223>

<400> 19
 aa aaa gtg atg gaa gag gcg aag gca ttc aca aca aat tat cta aag
 Lys Val Met Glu Glu Ala Lys Ala Phe Thr Thr Asn Tyr Leu Lys
 1 5 10 15

aaa gtt tta gca gga cgg gag gct acc cac gtc gat gaa agc ctt ttg

47

95

Lys	Val	Leu	Ala	Gly	Arg	Glu	Ala	Thr	His	Val	Asp	Glu	Ser	Leu	Leu		
				20					25					30			
gga	gag	gtg	aag	tac	gca	ttg	gag	ttt	cca	tgg	cat	tgc	agt	gtg	cag		143
Gly	Glu	Val	Lys	Tyr	Ala	Leu	Glu	Phe	Pro	Trp	His	Cys	Ser	Val	Gln		
			35					40					45				
aga	tgg	gag	gca	agg	agc	ttt	atc	gaa	ata	ttt	gga	caa	att	gat	tca		191
Arg	Trp	Glu	Ala	Arg	Ser	Phe	Ile	Glu	Ile	Phe	Gly	Gln	Ile	Asp	Ser		
		50					55					60					
gag	ctt	aag	tcg	aat	ttg	agc	aaa	aaa	atg	tta	gag	ttg	gcg	aaa	ttg		239
Glu	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Lys	Met	Leu	Glu	Leu	Ala	Lys	Leu		
	65					70					75						
gac	ttc	aat	att	ctg	caa	tgc	aca	cat	cag	aaa	gaa	ctg	cag	att	atc		287
Asp	Phe	Asn	Ile	Leu	Gln	Cys	Thr	His	Gln	Lys	Glu	Leu	Gln	Ile	Ile		
80					85				90						95		
tca	agg	tgg	ttc	gca	gac	tca	agt	ata	gca	tcc	ctg	aat	ttc	tat	cgg		335
Ser	Arg	Trp	Phe	Ala	Asp	Ser	Ser	Ile	Ala	Ser	Leu	Asn	Phe	Tyr	Arg		
				100					105					110			
aaa	tgt	tac	gtc	gaa	ttt	tac	ttt	tgg	atg	gct	gca	gcc	atc	tcc	gag		383
Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile	Ser	Glu		
			115					120					125				
ccg	gag	ttt	tct	gga	agc	aga	gtt	gcc	ttc	aca	aaa	att	gct	ata	ctg		431
Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu		
		130					135					140					
atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	ttg	gac	caa		479
Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln		
	145					150					155						
ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tgg	gat	gtt	tcg	ttg	gta		527
Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val		
160					165				170						175		
gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tgg	tta	aag		575
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys		
			180						185					190			
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat		623
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp		
			195				200					205					
atg	gcg	gcc	tac	ata	aga	aaa	aat	gca	tgg	gag	cga	tac	ctt	gaa	gct		671
Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Leu	Glu	Ala		
		210					215					220					
tat	ctg	caa	gat	gcg	gaa	tgg	ata	gcc	act	gga	cat	gtc	ccc	acc	ttt		719
Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe		
	225					230				235							
gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg		767
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu		
240				245					250					255			
aat	ttg	att	ccg	ctt	ctg	tta	atg	ggt	gaa	cat	tta	cca	atc	gac	att		815
Asn	Leu	Ile	Pro	Leu	Leu	Leu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile		

Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu
50 55 60

Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp
65 70 75 80

Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser
85 90 95

Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys
100 105 110

Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro
115 120 125

Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met
130 135 140

Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu
145 150 155 160

Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu
165 170 175

Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr
180 185 190

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer E

<220>
<221> misc_feature
<222> (1)..(23)
<223> Wherein N=inosine residue

<400> 21
ggngaramrr tnatggarga rgc

23

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate Oligonucleotide Primer F

<220>
<221> misc_feature
<222> (1)..(24)
<223> Wherein N=inosine residue

<400> 22

garytncary tnhbnmgntg gtgg

24

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate Oligonucleotide Primer G

<220>
<221> misc_feature
<222> (1)..(21)
<223> Wherein N=inosine residue

<400> 23
ccarttnarn ccytnacrt c

21

<210> 24
<211> 533
<212> DNA
<213> Abies Grandis

<400> 24
ggggaaaaaa tgatggagga agctgaaatc ttctctacca aatattttaa agaagccctg 60
caaaagattc cggctctccag tctttcgcga gagatcgggg acgttttggg atatggttgg 120
cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtctttgg acaggacact 180
gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240
aacatctttc aatccttact cgcataatcc cattgcaacc cattctgaca atggacatcc 300
cctttctctga tcatatcctc aaggaagttg acttcccatc aaagcttaac gacttggcat 360
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420
aagaagcttc ctctatatca tgttatatga aagacaatcc tggagtatca gaggaagatg 480
ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttcaat tgg 533

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid Motif on Which the Sequence of Primer D is based

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein Xaa=THR or ILE

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein Xaa=ILE or TYR or PHE

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=ALA or VAL

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Wherein Xaa=ALA or GLY

<400> 25

Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid Motif on Which the Sequence of Primer E is based

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein Xaa=LYS or THR

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein Xaa=VAL or ILE

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=GLU or ASP

<400> 26

Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid on Which the Sequence of Primer F is based

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Wherein Xaa=PHE or TYR or ASP

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein Xaa=ILE or LEU

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein Xaa=THR or LEU or ARG

<400> 27

Gln Xaa Xaa Xaa Arg Trp Trp
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved Amino Acid Motif on Which the Sequence of Primer G is based

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=PHE or LEU

<400> 28

Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> T3 Primer Oligonucleotide

<400> 29
aattaaccct cactaaaggg

<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7 Primer Oligonucleotide

<400> 30
 gtaatacgac tcactatagg gc 22

<210> 31
 <211> 2205
 <212> DNA
 <213> Abies Grandis

<220>
 <221> CDS
 <222> (57)..(1943)
 <223>

<400> 31
 gttatcttga gcttcctcca tataggccaa cacatatcat atcaaaggga gcaaga atg 59
 Met
 1

gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107
 Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
 5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
 Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
 20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
 Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser Met
 35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
 Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
 50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
 Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
 70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
 Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
 85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
 Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
 100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
 Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
 115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491

Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu	
130 135 140 145	
ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc	539
Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly	
150 155 160	
att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg	587
Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala	
165 170 175	
ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag	635
Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro Glu	
180 185 190	
gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta tgc tcc ccc	683
Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser Pro	
195 200 205	
ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta tat cgg gct	731
Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg Ala	
210 215 220 225	
tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa gct gaa atc	779
Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile	
230 235 240	
ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att cca gtc tcc	827
Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val Ser	
245 250 255	
gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc tgg cac aca	875
Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His Thr	
260 265 270	
aat ttg cca aga ttg gaa gca aga aat tac ata gac aca ctt gag aaa	923
Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu Lys	
275 280 285	
gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag ctt tta gaa	971
Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu Glu	
290 295 300 305	
ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa caa aag gaa	1019
Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys Glu	
310 315 320	
tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg cct aaa ttg	1067
Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys Leu	
325 330 335	
aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg gcc tct tgt	1115
Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser Cys	
340 345 350	
att gcc att gac cca aaa cat tct gca ttc aga cta ggc ttc gcc aaa	1163
Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys	
355 360 365	
atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac act ttt gga	1211
Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly	

370	375	380	385	
acg att gac gag ctt gaa ctc ttc aca tct gca att aag aga tgg aat				1259
Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp Asn				
390		395	400	
tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt gtg tac atg				1307
Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr Met				
405		410	415	
gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg gag aag act				1355
Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys Thr				
420		425	430	
caa ggg aga aac act ctc aac tat gtt cga aag gct tgg gag gct tat				1403
Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala Tyr				
435		440	445	
ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat ggt tat ctg				1451
Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr Leu				
450		455	460	465
cca acg ttt gaa gag tac cat gag aat ggg aaa gtg agc tct gca tat				1499
Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala Tyr				
470		475	480	
cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca tgg ctt cct				1547
Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu Pro				
485		490	495	
gat tac atc ttg aag gga att gat ttt cca tcc agg ttc aat gat ttg				1595
Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu				
500		505	510	
gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc tac aag gcc				1643
Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala				
515		520	525	
gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt tat atg aaa				1691
Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys				
530		535	540	545
gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat atc aat gcc				1739
Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala				
550		555	560	
atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt cta aga tcc				1787
Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg Ser				
565		570	575	
aac gac aat att cca atg ctg gcc aag aaa cat gct ttt gac ata aca				1835
Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile Thr				
580		585	590	
aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt agt gtt gcc				1883
Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val Ala				
595		600	605	
aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt gaa tct atg				1931
Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser Met				
610		615	620	625

ctt ttt taa cta taaccatata cataataata agctcataat gctaaattat 1983
 Leu Phe Leu

tggccttatg acatagttta tgtatgtact tgtgtgaatt caatcatata gtgtgggtat 2043
 gattaaaaag cttagagctta ctagggttagt aacatgggtga taaaagttat aaaatgtgag 2103
 ttatagagat acccatgttg aataatgaat tacaaaaaga gaaatttatg tagaataaga 2163
 ttggaagctt ttcaattggtt ttaaaaaaaaa aaaaaaaaaa aa 2205

<210> 32
 <211> 627
 <212> PRT
 <213> Abies Grandis

<400> 32

Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
 1 5 10 15

Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
 20 25 30

Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
 35 40 45

Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
 50 55 60

Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
 65 70 75 80

Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
 85 90 95

Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
 100 105 110

Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
 115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
 130 135 140

Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
 145 150 155 160

Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
165 170 175

Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
210 215 220

Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
225 230 235 240

Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270

Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
355 360 365

Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr

405

410

415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
420 425 430

Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
435 440 445

Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
450 455 460

Leu Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
465 470 475 480

Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
515 520 525

Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
530 535 540

Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
545 550 555 560

Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
565 570 575

Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
595 600 605

Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
610 615 620

Met Leu Phe
625

<210> 33

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 2.2 BamHI

<400> 33
caaagggatc cagaatggct ctgg 24

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 2.2 Not I

<400> 34
agtaagcggc cgctttttaa tcataccac 30

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 3.18 EcoRI

<400> 35
ctgcaggaat tcggcacgag c 21

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 3.18 SmaI

<400> 36
catagccccg ggcatagatt tgagctg 27

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Oligonucleotide Primer 10 NdeI

<400> 37
ggcaggaaca tatggctctc ctttctatcg 30

<210> 38
<211> 30
<212> DNA

gtcctcacat ggtaatatgt gagttgtgaa attctcaaaa aaaaaaaaaa aaaaaaaaaa 2103
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2163
 aaaaaaaaaa aaaaaaaaaa aaa 2186

<210> 67
 <211> 630
 <212> PRT
 <213> Abies Grandis

<400> 67

Met Ala Leu Val Ser Ser Ala Pro Lys Ser Cys Leu His Lys Ser Leu
 1 5 10 15

Ile Arg Ser Thr His His Glu Leu Lys Pro Leu Arg Arg Thr Ile Pro
 20 25 30

Thr Leu Gly Met Cys Arg Arg Gly Lys Ser Phe Thr Pro Ser Val Ser
 35 40 45

Met Ser Leu Thr Thr Ala Val Ser Asp Asp Gly Leu Gln Arg Arg Ile
 50 55 60

Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu
 65 70 75 80

Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Arg Glu Arg Ala Glu Lys Leu
 85 90 95

Ile Gly Glu Val Lys Glu Met Phe Asn Ser Met Pro Ser Glu Asp Gly
 100 105 110

Glu Ser Met Ser Pro Leu Asn Asp Leu Ile Glu Arg Leu Trp Met Val
 115 120 125

Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile
 130 135 140

Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu Lys Gly Ile
 145 150 155 160

Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser
 165 170 175

Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val
 180 185 190

Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser
195 200 205

Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser
210 215 220

Phe Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe
225 230 235 240

Ser Ser Arg Tyr Leu Lys Glu Ala Val Gln Lys Ile Pro Val Ser Ser
245 250 255

Leu Ser Gln Glu Ile Asp Tyr Thr Leu Glu Tyr Gly Trp His Thr Asn
260 265 270

Met Pro Arg Leu Glu Thr Arg Asn Tyr Leu Asp Val Phe Gly His Pro
275 280 285

Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Glu
290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly
325 330 335

Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr
340 345 350

Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu
355 360 365

Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val
385 390 395 400

Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys
405 410 415

Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu
420 425 430

Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala
435 440 445

Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val
465 470 475 480

Ser Ser Gly His Arg Ala Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp
485 490 495

Val.Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg
500 505 510

Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser
530 535 540

Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn
545 550 555 560

His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu
565 570 575

Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala
580 585 590

Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val
610 615 620

Leu Glu Pro Val Pro Leu
625 630

<210> 68
<211> 2429
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (35)..(1945)
<223>

<400> 68

attaaagaag ctaccatagt ttaggcagga atgc atg gct ctc ctt tct atc gta	55
Met Ala Leu Leu Ser Ile Val	
1 5	
tct ttg cag gtt ccc aaa tcc tgc ggg ctg aaa tcg ttg atc agt tcc	103
Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser	
10 15 20	
agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc	151
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu	
25 30 35	
aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc	199
Arg Met Arg Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr	
40 45 50 55	
act gta tcc cat cgt gat gat aat ggt ggt ggt gta ctg caa aga cgc	247
Thr Val Ser His Arg Asp Asp Asn Gly Gly Gly Val Leu Gln Arg Arg	
60 65 70	
ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca	295
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser	
75 80 85	
ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca	343
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr	
90 95 100	
gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga	391
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg	
105 110 115	
gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg	439
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val	
120 125 130 135	
gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata	487
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile	
140 145 150	
aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc	535
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly	
155 160 165	
att ggg tgt ggc aga gat tct act ttt cct gat ctc aac tcg act gct	583
Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala	
170 175 180	
ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat	631
Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp	
185 190 195	
gtg ctg gaa tac ttc aaa gat caa aag ggg cat ttt gcc tgc cct gca	679
Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala	
200 205 210 215	
atc cta acc gag gga cag atc act aga agt gtt cta aat tta tat cgg	727
Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg	

220										225					230					
gct	tcc	ctg	gtc	gcc	ttt	ccg	ggg	gag	aaa	ggt	atg	gaa	gag	gct	gaa	775				
Ala	Ser	Leu	Val	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu					
235					240					245										
atc	ttc	tcg	gca	tct	tat	ttg	aaa	gaa	gtc	tta	caa	aag	att	cca	gtc	823				
Ile	Phe	Ser	Ala	Ser	Tyr	Leu	Lys	Glu	Val	Leu	Gln	Lys	Ile	Pro	Val					
250					255					260										
tcc	agt	ttt	tca	cga	gag	ata	gaa	tac	ggt	ttg	gaa	tat	ggt	tgg	cac	871				
Ser	Ser	Phe	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Tyr	Gly	Trp	His					
265					270					275										
aca	aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tat	atc	gac	gtc	tac	ggg	919				
Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Val	Tyr	Gly					
280					285					290					295					
cag	gac	agc	tat	gaa	agt	tca	aac	gag	atg	cca	tat	gtg	aat	acg	cag	967				
Gln	Asp	Ser	Tyr	Glu	Ser	Ser	Asn	Glu	Met	Pro	Tyr	Val	Asn	Thr	Gln					
300					305					310										
aag	ctt	tta	aaa	ctt	gca	aaa	ttg	gag	ttt	aat	atc	ttt	cac	tct	ttg	1015				
Lys	Leu	Leu	Lys	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu					
315					320					325										
caa	cag	aaa	gag	ttg	caa	tat	atc	tct	aga	tgg	tgg	aaa	gat	tcg	tgt	1063				
Gln	Gln	Lys	Glu	Leu	Gln	Tyr	Ile	Ser	Arg	Trp	Trp	Lys	Asp	Ser	Cys					
330					335					340										
tca	tct	cat	ctg	act	ttt	act	cga	cac	cgt	cac	gtg	gaa	tac	tac	aca	1111				
Ser	Ser	His	Leu	Thr	Phe	Thr	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr					
345					350					355										
atg	gca	tct	tgc	att	tct	atg	gag	ccg	aaa	cac	tcc	gct	ttc	aga	ttg	1159				
Met	Ala	Ser	Cys	Ile	Ser	Met	Glu	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu					
360					365					370					375					
ggg	ttt	gtc	aaa	aca	tgt	cat	ctt	cta	aca	ggt	ctg	gat	gat	atg	tat	1207				
Gly	Phe	Val	Lys	Thr	Cys	His	Leu	Leu	Thr	Val	Leu	Asp	Asp	Met	Tyr					
380					385					390										
gac	act	ttt	gga	aca	ctg	gac	gaa	ctc	caa	ctt	ttt	acg	act	gcc	ttt	1255				
Asp	Thr	Phe	Gly	Thr	Leu	Asp	Glu	Leu	Gln	Leu	Phe	Thr	Thr	Ala	Phe					
395					400					405										
aag	aga	tgg	gat	ttg	tca	gag	aca	aag	tgt	ctt	cca	gaa	tat	atg	aaa	1303				
Lys	Arg	Trp	Asp	Leu	Ser	Glu	Thr	Lys	Cys	Leu	Pro	Glu	Tyr	Met	Lys					
410					415					420										
gca	gtg	tac	atg	gac	ttg	tat	caa	tgt	ctt	aat	gaa	ttg	gcg	caa	gag	1351				
Ala	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys	Leu	Asn	Glu	Leu	Ala	Gln	Glu					
425					430					435										
gct	gag	aag	act	caa	ggc	aga	gat	acg	ctc	aac	tat	att	cgc	aat	gct	1399				
Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Thr	Leu	Asn	Tyr	Ile	Arg	Asn	Ala					
440					445					450					455					
tat	gag	tct	cat	ttt	gat	tcg	ttt	atg	cac	gaa	gca	aaa	tgg	atc	tca	1447				
Tyr	Glu	Ser	His	Phe	Asp	Ser	Phe	Met	His	Glu	Ala	Lys	Trp	Ile	Ser					
460					465					470										

agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Lys Asn Gly Lys Val 475 480 485	1495
agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp 490 495 500	1543
gta cca ctt cct aat tac ata ctg caa gaa att gat tat cca tct agg Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg 505 510 515	1591
ttc aat gac ttg gct tcg tcc ctc ctt cgg cta cgt ggt gac acg cgc Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg 520 525 530 535	1639
tgc tac aag gcg gat agg gct cgt gga gaa gaa gct tca gct ata tcg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser 540 545 550	1687
tgt tat atg aaa gac cat cct gga tca aca gag gaa gat gct ctc aat Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn 555 560 565	1735
cat atc aac gtc atg atc agt gat gca atc aga gaa tta aat tgg gag His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu 570 575 580	1783
ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala 585 590 595	1831
ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly 600 605 610 615	1879
tac act gtt gcg agt agt gaa aca aag aat ttg gtg atg aaa aca gtt Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val 620 625 630	1927
ctt gaa cct gtg gca ttg taaaaaata tcaaccgcat caaaatgcac Leu Glu Pro Val Ala Leu 635	1975
ggagtttgta atttaatgca cttctcttat aatacacttc tctttagacc tgtagtgaag	2035
ccgatgcacc attacagtgt atatgggagc cagtctagtc tcaaaaagtt tgtaaagtgt	2095
attctatgat atactcttta gaccaaagc tagatgcccc tgaaaagcaa gtgtttttaga	2155
attgcttctg gatttgctta aattttctcc atgattcttt agaaatgttg catccccaaa	2215
cttcactgcc atataagata acgggagtga caaggatttt aaagaggatt tttttttatg	2275
tcccgcacaa caaggtttgt cgatttacag ttgttttcaa gactgaagta ggatttccac	2335
cctccattaa tctcttctc gatgttatag ttctacttga gcttgtgatg gaagtcaatt	2395
cctagatatt tataagaaaa aaaaaaaaaa aaaa	2429

<210> 69
<211> 637
<212> PRT
<213> Abies Grandis

<400> 69

Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
1 5 10 15

Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg

210

215

220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
 225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Glu
 245 250 255

Val Leu Gln Lys Ile Pro Val Ser Ser Phe Ser Arg Glu Ile Glu Tyr
 260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg
 275 280 285

Asn Tyr Ile Asp Val Tyr Gly Gln Asp Ser Tyr Glu Ser Ser Asn Glu
 290 295 300

Met Pro Tyr Val Asn Thr Gln Lys Leu Leu Lys Leu Ala Lys Leu Glu
 305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr Ile Ser
 325 330 335

Arg Trp Trp Lys Asp Ser Cys Ser Ser His Leu Thr Phe Thr Arg His
 340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Glu Pro
 355 360 365

Lys His Ser Ala Phe Arg Leu Gly Phe Val Lys Thr Cys His Leu Leu
 370 375 380

Thr Val Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Leu Asp Glu Leu
 385 390 395 400

Gln Leu Phe Thr Thr Ala Phe Lys Arg Trp Asp Leu Ser Glu Thr Lys
 405 410 415

Cys Leu Pro Glu Tyr Met Lys Ala Val Tyr Met Asp Leu Tyr Gln Cys
 420 425 430

Leu Asn Glu Leu Ala Gln Glu Ala Glu Lys Thr Gln Gly Arg Asp Thr
 435 440 445

Leu Asn Tyr Ile Arg Asn Ala Tyr Glu Ser His Phe Asp Ser Phe Met
 450 455 460

His Glu Ala Lys Trp Ile Ser Ser Gly Tyr Leu Pro Thr Phe Glu Glu
465 470 475 480

Tyr Leu Lys Asn Gly Lys Val Ser Ser Gly Ser Arg Thr Ala Thr Leu
485 490 495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asn Tyr Ile Leu Gln
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser Leu Leu
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser
545 550 555 560

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

<210> 70

<211> 696

<212> DNA

<213> Abies grandis

<400> 70

gcatttaaga gatgggatcc gtctgccaca gatttgcttc cagagtatat gaaagggttg	60
tacatggtgg tttaacgaaac cgtaaatgaa attgctcgag aggcagacaa gtctcaaggc	120
cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa	180
gaagctgagt ggatctccag tggttatctg ccaacgtttg aggagtacat ggagaccagc	240
aaagttagtt ttggttatcg catattcgca ttgcaaccca tcctcactat ggatgttccc	300

<400> 74

actcactata gggctcgagc ggc

23

<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer AG9F

<400> 75
atggctcttg tttctatctt gccc

24

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer AG9R

<400> 76
ttacaaaggc acagactcaa ggac

24

<210> 77
<211> 1890
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (1)..(1890)
<223>

<400> 77
atg gct ctt gtt tct atc ttg ccc ttg tct tcc aaa tcg gtc ctg cac
Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

48

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

96

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

144

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

192

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata
Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
65 70 75 80

240

caa tct cta tca acg cct tat ggg gca cct tca tac cgt gaa cgt gct
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala

288

85								90				95					
gat	aga	ctt	att	gtg	gaa	gta	aag	ggg	ata	ttc	act	tca	att	tca	gcg	336	
Asp	Arg	Leu	Ile	Val	Glu	Val	Lys	Gly	Ile	Phe	Thr	Ser	Ile	Ser	Ala		
			100					105					110				
gaa	gat	gga	gaa	cta	atc	act	ccc	ctc	aat	gat	ctc	att	caa	cgc	ctt	384	
Glu	Asp	Gly	Glu	Leu	Ile	Thr	Pro	Leu	Asn	Asp	Leu	Ile	Gln	Arg	Leu		
		115					120					125					
tta	atg	gtc	gat	aac	gtt	gaa	cgt	tta	ggg	att	gat	aga	cat	ttc	aaa	432	
Leu	Met	Val	Asp	Asn	Val	Glu	Arg	Leu	Gly	Ile	Asp	Arg	His	Phe	Lys		
	130					135					140						
aat	gag	ata	aaa	gca	gca	cta	gac	tat	gtt	tac	agt	tat	tgg	aac	gaa	480	
Asn	Glu	Ile	Lys	Ala	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	Tyr	Trp	Asn	Glu		
145				150						155					160		
aaa	ggc	att	ggc	agt	gga	agt	gat	agt	ggg	gtt	gct	gat	ctc	aac	tca	528	
Lys	Gly	Ile	Gly	Ser	Gly	Ser	Asp	Ser	Gly	Val	Ala	Asp	Leu	Asn	Ser		
			165					170					175				
act	gcc	ctg	ggg	ttt	cga	att	ctt	cga	cta	cac	gga	tac	agt	gtt	tct	576	
Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Leu	His	Gly	Tyr	Ser	Val	Ser		
		180					185						190				
tca	gat	gtg	ttg	gaa	cac	ttc	aaa	gag	gag	aag	gag	aag	ggg	cag	ttt	624	
Ser	Asp	Val	Leu	Glu	His	Phe	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Gln	Phe		
		195					200					205					
gta	tgt	tcg	gcc	atc	caa	aca	gag	gaa	gag	ata	aaa	agc	gtt	ctg	aat	672	
Val	Cys	Ser	Ala	Ile	Gln	Thr	Glu	Glu	Glu	Ile	Lys	Ser	Val	Leu	Asn		
	210					215					220						
tta	ttt	cgg	gcc	tcc	ctc	att	gcc	ttt	cct	ggg	gag	aaa	gtt	atg	gaa	720	
Leu	Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu		
225				230					235					240			
gag	gct	gaa	atc	ttc	tct	aaa	ata	tat	tta	aaa	gaa	gcc	tta	caa	aat	768	
Glu	Ala	Glu	Ile	Phe	Ser	Lys	Ile	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Asn		
			245					250					255				
att	gct	gtc	tcc	agt	ctt	tca	cga	gag	ata	gag	tac	gtt	ctg	gag	gat	816	
Ile	Ala	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Asp		
		260					265					270					
ggg	tgg	caa	aca	aat	atg	cca	aga	ttg	gaa	aca	agg	aac	tac	atc	gat	864	
Gly	Trp	Gln	Thr	Asn	Met	Pro	Arg	Leu	Glu	Thr	Arg	Asn	Tyr	Ile	Asp		
		275				280					285						
gta	ttg	gga	gag	aac	gat	cgt	gat	gag	acg	tta	tat	atg	aac	atg	gag	912	
Val	Leu	Gly	Glu	Asn	Asp	Arg	Asp	Glu	Thr	Leu							

ttc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct	1056
Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala	
340 345 350	
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc	1104
Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu	
355 360 365	
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac	1152
Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr	
370 375 380	
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt	1200
Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe	
385 390 395 400	
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa	1248
Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys	
405 410 415	
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag	1296
Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu	
420 425 430	
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct	1344
Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala	
435 440 445	
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc	1392
Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser	
450 455 460	
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt	1440
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val	
465 470 475 480	
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat	1488
Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp	
485 490 495	
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg	1536
Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg	
500 505 510	
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc	1584
Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg	
515 520 525	
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg	1632
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser	
530 535 540	
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat	1680
Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn	
545 550 555 560	
cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag	1728
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu	
565 570 575	

ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct 1776
 Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
 580 585 590

ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg 1824
 Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
 595 600 605

ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc 1872
 Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
 610 615 620

ctt gag tct gtg cct ttg 1890
 Leu Glu Ser Val Pro Leu
 625 630

<210> 78
 <211> 630
 <212> PRT
 <213> Abies Grandis

<400> 78

Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
 1 5 10 15

Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
 20 25 30

Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
 35 40 45

Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
 50 55 60

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
 65 70 75 80

Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
 85 90 95

Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala
 100 105 110

Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu
 115 120 125

Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys
 130 135 140

Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu

145

150

155

160

Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser
 165 170 175

Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser
 180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe
 195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn
 210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu
 225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn
 245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp
 260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp
 275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu
 290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
 305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly
 325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala
 340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu
 355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
 370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe
 385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg
500 505 510

Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser
530 535 540

Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn
545 550 555 560

His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu
565 570 575

Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
580 585 590

Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
610 615 620

Leu Glu Ser Val Pro Leu
625 630

<210> 79
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Mutagenesis Primer 6eBamHIF

 <400> 79
 caattaagag atgggacccg tccgcgatgg 30

<210> 80
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Mutagenesis Primer 6eBamHIR

 <400> 80
 ccatcgcgga cgggtcccat ctcttaattg 30

<210> 81
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Mutagenesis Primer 9eBamHIF

 <400> 81
 gcatttaaga gatgggaccc gtctgccaca 30

<210> 82
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Mutagenesis Primer 9eBamHIR

 <400> 82
 ctgtggcaga cgggtcccat ctcttaaattg 30

<210> 83
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Mutagenesis Primer 732eNdeIF

 <400> 83
 cgagatgccg tacgtgaata cgcag 25

<210> 84
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Mutagenesis Primer 732eNde1R

<400> 84
ctgcgtattc acgtatggca tctcg 25

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer 6-Nde1-M

<400> 85
ctgatatgcaa gctcatatgg ctcttctttc 30

<210> 86
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer 6-NdeI-R

<400> 86
gccacgcgt ctcatatgag aatcagtaga tgcg 34

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer 6-BamHI

<400> 87
cacccatagg ggatcctcag ttaatattg 29

<210> 88
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide PCR Primer 8-NdeI-M

<400> 88
taagcgagca catatggctc tggtttcttc 30

<210> 89

<211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 8-BamHI

 <400> 89
 gcataaacgc atagcggatc ctacaccaa 29

 <210> 90
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 9-NdeI-M

 <400> 90
 cccggggatc ggacatatgg ctcttgtttc 30

 <210> 91
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 9-BamHI

 <400> 91
 ggtcgactct agaggatcca ctagtgatat ggat 34

 <210> 92
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 11-NdeI-M

 <400> 92
 gaacatatgg ctctcctttc tatcgta 27

 <210> 93
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 11-NdeI-R

 <400> 93
 ggtggtggtg tacatatgag acgcatacgg g 31

 <210> 94
 <211> 34

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 11-BamHI

 <400> 94
 gagactagac tggatcccat atacactgta atgg 34

 <210> 95
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 2-NdeI-M

 <400> 95
 caaagggagc acatatggct ctgg 24

 <210> 96
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 2-NdeI-R

 <400> 96
 ctgatgatgg tcatatgaga cgcataggtg 30

 <210> 97
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 2-BamHI

 <400> 97
 gaccttatta ttatggatcc gggttatag 28

 <210> 98
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide PCR Primer 3NdeI-R

 <400> 98
 ccgatgatgg tcatatgaga cgcatgggcg 30

 <210> 99
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide PCR Primer 3-BamHI

<400> 99

gggcatagat ttgagcggat cctacaaagg

30

<210> 100

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Mutagenesis Primer 3elBamHIF

<400> 100

cgtttgggaa tccatagaca tttc

24

<210> 101

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Mutagenesis Primer 3elBamHIR

<400> 101

gaaatgtcta tggattccca aacg

24

<210> 102

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide PCR Primer 3e2BamHIF

<400> 102

gaagagatgg gaccgcgcct cgatag

26

<210> 103

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide PCR Primer 2-NdeI-M

<400> 103

ctatcgagga cgggtcccat ctcttc

26

<210> 104

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Mutagenesis Primer 3e1NdeIF

<400> 104

gaacacgaag tcctatgtga agagc

25

<210> 105

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Mutagenesis Primer 3e1NdeIR

<400> 105

gctcttcaca taggacttcg tgttc

25

<210> 106

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Mutagenesis Primer 3e3NdeIF

<400> 106

gatacgctca cttatgctcg ggaag

25

<210> 107

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Mutagenesis Primer 3e2NdeIR

<400> 107

cttcccgcgc ataagtgagc gtatc

25

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Primer 10 BamHI

<400> 38

tctagaacta gtggatcccc cgggctgcag

30

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Primer JB29

<400> 39

ctaccattcc aatatctg

18

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Primer 2-8

<400> 40

gttggatcctt agaagttccc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Primer 3-9

<400> 41

tttccattcc aacctctggg

20

<210> 42

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Primer 3-11

<400> 42

cgtaatggaa agctctggcg

20

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Primer 7-1

<400> 43

ccttacacgc ctttggatgg

20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Oligonucleotide Sequence 7-3

<400> 44

tctgttgatc caggatggtc

20

<210> 45

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved Amino Acid Motif Common to All Prenyl Transferases

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> Wherein Xaa=any amino acid

<400> 45

Asp Asp Xaa Xaa Asp

1

5

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid Motif from which Oligonucleotide Primers can be Synthesized that Hybridize to the Monoterpene Synthases of the Present Invention

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Wherein Xaa=LEU or ILE or VAL

<400> 46

His Ser Asn Xaa Thr Asp Asp Asp

1

5

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Degenerate Oligonucleotides can be Constructed that Hybridize to the Monoterpene Synthases of the Present Invention

<400> 47

Ala Leu Asp Tyr Val Tyr
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Degenerate Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthases of the Present Invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Degenerate Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<400> 49

Arg Trp Trp Lys Glu Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<220>
<221> MISC_FEATURE

<222> (1)..(1)
<223> Wherein Xaa=VAL or ILE or LEU

<400> 50

Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein Xaa=VAL or ILE or LEU

<400> 51

Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Oligonucleotide Sequences can be Constructed that Hybridize to the Monoterpene Synthase Clones of the Present Invention

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein Xaa=VAL or ILE or LEU

<400> 52

Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Motif from which Oligonucleotide Sequences can be Cons

tructed that Hybridize to the Monoterpene Synthase Clones of the
Present Invention

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Wherein Xaa=ASN or HIS

<400> 53

Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Oligonucleotide that Corresponds to Peptide Sequence Me
tMetMet

<400> 54
atgatgatg 9

<210> 55
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Oligonucleotide Sequence that Corresponds to Peptide Se
quence MetMetMet

<400> 55
tactactac 9

<210> 56
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Oligonucleotide that Corresponds to Peptide Sequence Me
tMetMet

<220>
<221> misc_feature
<222> (1)..(9)
<223> Wherein N=inosine

<400> 56
nacnacnac 9

<210> 57

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Corresponding to Amino Acid Sequence Set Forth in
 SEQ ID NO:46

 <400> 57
 gtgtcgttgg agaccctgct gctg 24

 <210> 58
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Corresponding to Amino Acid Sequence Set Forth in
 SEQ ID NO:47

 <400> 58
 cgggagctga tgcagatg 18

 <210> 59
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Corresponding to Conserved Amino Acid Sequence Se
 t Forth in SEQ ID NO:48

 <400> 59
 ctcgagcggt tcgagctcaa g 21

 <210> 60
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Corresponding to Conserved Amino Acid Sequence Se
 t Forth in SEQ ID NO:49

 <400> 60
 gccaccacct tcctctcg 18

 <210> 61
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Sequence Corresponding to Amino Acid Sequence Set
 Forth in SEQ ID NO:50

 <400> 61

gaggagctgc tgtacatgct g

21

<210> 62

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Corresponding to Conserved Amino Acid Sequence Set Forth in SEQ ID NO:51

<400> 62

gaggagctgc tggagatgct g

21

<210> 63

<211> 293

<212> DNA

<213> Abies Grandis

<400> 63

cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgct caactatatt 60

cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

ggttatctcc caacgtttga ggagtacttg aagaatggga aagttagttc cggttctcgc 180

acagccactt tacaacccat actcaccttg gatgtaccac ttcctaatta catactgcaa 240

gaaattgatt atccatctag gttcaatgac ttggcttcgt ccttccttcg cta 293

<210> 64

<211> 2013

<212> DNA

<213> Abies Grandis

<220>

<221> CDS

<222> (36)..(1889)

<223>

<400> 64

ttttgacgtg ccttcttattc tgatagcaag ctgaa atg gct ctt ctt tct att 53
Met Ala Leu Leu Ser Ile
1 5

act ccg ctg gtt tcc agg tcg tgc ctc agt tct tct cat gag att aag 101
Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser Ser His Glu Ile Lys
10 15 20

gct ctc cgt aga aca atc cca act ctt gga atc tgc agg ccg ggg aaa 149
Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys
25 30 35

tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197
Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr
40 45 50

gat tct gta cag aga cgc gtg ggc aac tat cat tcc aac ctg tgg gac	245
Asp Ser Val Gln Arg Arg Val Gly Asn Tyr His Ser Asn Leu Trp Asp	
55 60 65 70	
gat gat ttc ata cag tct ctg atc tca acg cct tat gga gca cct gat	293
Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr Pro Tyr Gly Ala Pro Asp	
75 80 85	
tac cgg gaa cgt gct gac aga ctt att ggg gaa gta aag gat ata atg	341
Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly Glu Val Lys Asp Ile Met	
90 95 100	
ttc aat ttc aag tcg ctg gaa gat gga ggc aat gat ctc ctt caa cga	389
Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly Asn Asp Leu Leu Gln Arg	
105 110 115	
ctt ttg ctg gtc gat gac gtt gaa cgt ttg gga atc gac agg cat ttc	437
Leu Leu Leu Val Asp Asp Val Glu Arg Leu Gly Ile Asp Arg His Phe	
120 125 130	
aaa aaa gag ata aaa acg gca ctc gat tat gtt aac agt tat tgg aac	485
Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr Val Asn Ser Tyr Trp Asn	
135 140 145 150	
gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac	533
Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn	
155 160 165	
tca acc gcc ttg ggg ctt cga act ctc cga cta cac gga tac act gtg	581
Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Thr Val	
170 175 180	
tct tca gat gtt ttg aac gtt ttt aaa gac aaa aat ggg caa ttt tcc	629
Ser Ser Asp Val Leu Asn Val Phe Lys Asp Lys Asn Gly Gln Phe Ser	
185 190 195	
tcc act gcc aat att cag ata gag gga gag att aga ggc gtt ctc aat	677
Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu Ile Arg Gly Val Leu Asn	
200 205 210	
tta ttc agg gcc tcc ctc gtc gcc ttt ccc ggc gag aaa gtt atg gat	725
Leu Phe Arg Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Asp	
215 220 225 230	
gaa gct gaa aca ttc tct aca aaa tat tta aga gaa gcc ctg caa aag	773
Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu Arg Glu Ala Leu Gln Lys	
235 240 245	
att ccg gca tcc agt ata ctt tca cta gag ata ccg gac gtt ctg gaa	821
Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu Ile Arg Asp Val Leu Glu	
250 255 260	
tat ggt tgg cac acc aat ttg cca cgc ttg gaa gca agg aat tac atg	869
Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Met	
265 270 275	
gac gtc ttt gga cag cac act aaa aat aag aac gcc gcc gag aaa ctt	917
Asp Val Phe Gly Gln His Thr Lys Asn Lys Asn Ala Ala Glu Lys Leu	
280 285 290	
tta gaa ctt gca aaa ttg gaa ttc aat ata ttt cac tcc tta caa gag	965

Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu	Gln	Glu		
295					300					305					310		
aga	gag	tta	aaa	cat	gtt	tcc	cga	tgg	tgg	aaa	gac	tcg	ggg	tct	cct	1013	
Arg	Glu	Leu	Lys	His	Val	Ser	Arg	Trp	Trp	Lys	Asp	Ser	Gly	Ser	Pro		
				315					320					325			
gag	atg	acc	ttc	tgt	cga	cat	cgt	cac	gtg	gaa	tac	tac	gct	ttg	gct	1061	
Glu	Met	Thr	Phe	Cys	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Ala	Leu	Ala		
			330					335					340				
tcc	tgc	att	gcg	ttc	gag	cct	caa	cat	tct	gga	ttc	aga	ctc	ggc	ttt	1109	
Ser	Cys	Ile	Ala	Phe	Glu	Pro	Gln	His	Ser	Gly	Phe	Arg	Leu	Gly	Phe		
		345					350					355					
acc	aag	atg	tct	cat	ctt	atc	acg	gtt	ctt	gac	gac	atg	tac	gac	gtc	1157	
Thr	Lys	Met	Ser	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Met	Tyr	Asp	Val		
	360					365				370							
ttc	ggc	aca	gta	gac	gag	ctg	gaa	ctc	ttc	aca	gcg	aca	att	aag	aga	1205	
Phe	Gly	Thr	Val	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ala	Thr	Ile	Lys	Arg		
375					380				385						390		
tgg	gat	ccg	tcc	gcg	atg	gaa	tgc	ctt	cca	gaa	tat	atg	aaa	gga	gtg	1253	
Trp	Asp	Pro	Ser	Ala	Met	Glu	Cys	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val		
			395					400						405			
tac	atg	atg	gtt	tat	cac	acc	gta	aat	gaa	atg	gct	cga	gtg	gca	gag	1301	
Tyr	Met	Met	Val	Tyr	His	Thr	Val	Asn	Glu	Met	Ala	Arg	Val	Ala	Glu		
			410					415					420				
aag	gct	caa	ggc	cga	gac	acg	ctc	aac	tat	gca	aga	cag	gct	tgg	gag	1349	
Lys	Ala	Gln	Gly	Arg	Asp	Thr	Leu	Asn	Tyr	Ala	Arg	Gln	Ala	Trp	Glu		
		425					430					435					
gcg	tgt	ttt	gat	tcg	tat	atg	cag	gaa	gca	aag	tgg	atc	gcc	act	ggg	1397	
Ala	Cys	Phe	Asp	Ser	Tyr	Met	Gln	Glu	Ala	Lys	Trp	Ile	Ala	Thr	Gly		
	440					445					450						
tat	ctg	ccc	acg	ttt	gag	gag	tac	ttg	gag	aac	ggg	aaa	gtt	agc	tct	1445	
Tyr	Leu	Pro	Thr	Phe	Glu	Glu	Tyr	Leu	Glu	Asn	Gly	Lys	Val	Ser	Ser		
455					460				465						470		
gct	cat	cgc	cca	tgc	gca	ctg	caa	ccc	att	ctg	acg	ttg	gac	atc	ccc	1493	
Ala	His	Arg	Pro	Cys	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asp	Ile	Pro		
				475				480						485			
ttt	cct	gat	cac	atc	ctc	aag	gaa	gtt	gac	ttc	cca	tcg	aag	ctc	aat	1541	
Phe	Pro	Asp	His	Ile	Leu	Lys	Glu	Val	Asp	Phe	Pro	Ser	Lys	Leu	Asn		
			490					495					500				
gac	ttg	ata	tgt	atc	atc	ctt	cga	tta	aga	ggg	gat	aca	cgg	tgc	tac	1589	
Asp	Leu	Ile	Cys	Ile	Ile	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr		
		505					510					515					
aag	gca	gac	agg	gcc	cgt	gga	gaa	gaa	gct	tcg	tct	ata	tca	tgt	tat	1637	
Lys	Ala	Asp	Arg	Ala	Arg	Gly	Glu	Glu	Ala	Ser	Ser	Ile	Ser	Cys	Tyr		
		520				525					530						
atg	aaa	gac	aat	cct	gga	tta	acg	gaa	gaa	gat	gct	ctg	aat	cat	atc	1685	
Met	Lys	Asp	Asn	Pro	Gly	Leu	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile		

535	540	545	550	
aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta				1733
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu				
555		560	565	
aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac				1781
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp				
570		575	580	
ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc				1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser				
585		590	595	
ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa				1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu				
600		605	610	
cct gtg cct ttg taacaacact tcaaactctac aatattaact gaggatgccc				1929
Pro Val Pro Leu				
615				
tatgggtgta tatagggcac acaaaaataa atatggttgt gttagtaaag ctgtaattta				1989
tgaaaaaaaa aaaaaaaaaa aaaa				2013

<210> 65
 <211> 618
 <212> PRT
 <213> Abies Grandis

<400> 65

Met Ala Leu Leu Ser Ile Thr Pro Leu Val Ser Arg Ser Cys Leu Ser			
1	5	10	15
Ser Ser His Glu Ile Lys Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly			
20	25	30	
Ile Cys Arg Pro Gly Lys Ser Val Ala His Ser Ile Asn Met Cys Leu			
35	40	45	
Thr Ser Val Ala Ser Thr Asp Ser Val Gln Arg Arg Val Gly Asn Tyr			
50	55	60	
His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr			
65	70	75	80
Pro Tyr Gly Ala Pro Asp Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly			
85	90	95	
Glu Val Lys Asp Ile Met Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly			
100	105	110	

Asn Asp Leu Leu Gln Arg Leu Leu Leu Val Asp Asp Val Glu Arg Leu
115 120 125

Gly Ile Asp Arg His Phe Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr
130 135 140

Val Asn Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser
145 150 155 160

Val Val Thr Asp Leu Asn Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg
165 170 175

Leu His Gly Tyr Thr Val Ser Ser Asp Val Leu Asn Val Phe Lys Asp
180 185 190

Lys Asn Gly Gln Phe Ser Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu
195 200 205

Ile Arg Gly Val Leu Asn Leu Phe Arg Ala Ser Leu Val Ala Phe Pro
210 215 220

Gly Glu Lys Val Met Asp Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu
225 230 235 240

Arg Glu Ala Leu Gln Lys Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu
245 250 255

Ile Arg Asp Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu
260 265 270

Glu Ala Arg Asn Tyr Met Asp Val Phe Gly Gln His Thr Lys Asn Lys
275 280 285

Asn Ala Ala Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile
290 295 300

Phe His Ser Leu Gln Glu Arg Glu Leu Lys His Val Ser Arg Trp Trp
305 310 315 320

Lys Asp Ser Gly Ser Pro Glu Met Thr Phe Cys Arg His Arg His Val
325 330 335

Glu Tyr Tyr Ala Leu Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser
340 345 350

Gly Phe Arg Leu Gly Phe Thr Lys Met Ser His Leu Ile Thr Val Leu
355 360 365

Asp Asp Met Tyr Asp Val Phe Gly Thr Val Asp Glu Leu Glu Leu Phe
370 375 380

Thr Ala Thr Ile Lys Arg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro
385 390 395 400

Glu Tyr Met Lys Gly Val Tyr Met Met Val Tyr His Thr Val Asn Glu
405 410 415

Met Ala Arg Val Ala Glu Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr
420 425 430

Ala Arg Gln Ala Trp Glu Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala
435 440 445

Lys Trp Ile Ala Thr Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu
450 455 460

Asn Gly Lys Val Ser Ser Ala His Arg Pro Cys Ala Leu Gln Pro Ile
465 470 475 480

Leu Thr Leu Asp Ile Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp
485 490 495

Phe Pro Ser Lys Leu Asn Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg
500 505 510

Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala
515 520 525

Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu
530 535 540

Asp Ala Leu Asn His Ile Asn Phe Met Ile Arg Asp Ala Ile Arg Glu
545 550 555 560

Leu Asn Trp Glu Leu Leu Lys Pro Asp Asn Ser Val Pro Ile Thr Ser
565 570 575

Lys Lys His Ala Phe Asp Ile Ser Arg Val Trp His His Gly Tyr Arg
580 585 590

Tyr Arg Asp Gly Tyr Ser Phe Ala Asn Val Glu Thr Lys Ser Leu Val

Met Arg Thr Val Ile Glu Pro Val Pro Leu
610 615

<210> 66
<211> 2186
<212> DNA
<213> Abies Grandis

<220>
<221> CDS
<222> (34)..(1923)
<223>

<400> 66

```

cccaaattcct atatccgtta taagcgagca gga atg gct ctg gtt tct tcc gca      54
                               Met Ala Leu Val Ser Ser Ala
                               1           5

ccc aaa tcc tgc ctg cac aaa tcg ttg atc agg tct act cat cat gag      102
Pro Lys Ser Cys Leu His Lys Ser Leu Ile Arg Ser Thr His His Glu
      10           15           20

ctc aag cct ctg cgc aga acc atc cca act ctt gga atg tgt agg cga      150
Leu Lys Pro Leu Arg Arg Thr Ile Pro Thr Leu Gly Met Cys Arg Arg
      25           30           35

ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta      198
Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val
      40           45           50           55

tct gat gat ggt cta caa aga cgc ata ggt gac tat cat tcc aat ctc      246
Ser Asp Asp Gly Leu Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Leu
      60           65           70

tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct      294
Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro
      75           80           85

tct tac cga gaa cgt gct gag aaa ctg att ggg gaa gtg aag gag atg      342
Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met
      90           95           100

ttc aat tca atg cca tcg gaa gat gga gaa tca atg agt ccc ctc aat      390
Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn
      105           110           115

gat ctt att gaa cga ctt tgg atg gtc gat agc gtt gaa cgt ttg ggg      438
Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly
      120           125           130           135

att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt      486
Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val
      140           145           150

tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt      534
Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val

```

155	160	165	
ttt cct gat gtc aac tcg act ggc tcg ggg ttt cga act ctt cgc cta Phe Pro Asp Val Asn Ser Thr Ala Ser Gly Phe Arg Thr Leu Arg Leu 170 175 180			582
cac gga tac agt gtc tct tca gag gtt ttg aaa gta ttt caa gac caa His Gly Tyr Ser Val Ser Ser Glu Val Leu Lys Val Phe Gln Asp Gln 185 190 195			630
aat ggg cag ttt gca ttc tct cct agt aca aaa gag aga gac atc aga Asn Gly Gln Phe Ala Phe Ser Pro Ser Thr Lys Glu Arg Asp Ile Arg 200 205 210 215			678
acc gtt ctg aat tta tat cgg gct tct ttc att gcc ttt cct ggg gag Thr Val Leu Asn Leu Tyr Arg Ala Ser Phe Ile Ala Phe Pro Gly Glu 220 225 230			726
aaa gtt atg gaa gag gct gaa att ttc tct tca aga tat ttg aaa gaa Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ser Arg Tyr Leu Lys Glu 235 240 245			774
gcc gtg caa aag att ccg gtc tcc agt ctt tca caa gaa ata gac tac Ala Val Gln Lys Ile Pro Val Ser Ser Leu Ser Gln Glu Ile Asp Tyr 250 255 260			822
act ttg gaa tat ggt tgg cac aca aat atg cca aga ttg gaa aca agg Thr Leu Glu Tyr Gly Trp His Thr Asn Met Pro Arg Leu Glu Thr Arg 265 270 275			870
aat tac tta gat gta ttt gga cat cct acc agt cca tgg ctc aag aag Asn Tyr Leu Asp Val Phe Gly His Pro Thr Ser Pro Trp Leu Lys Lys 280 285 290 295			918
aaa agg acg caa tat ctg gac agc gaa aag ctt tta gaa ctc gca aaa Lys Arg Thr Gln Tyr Leu Asp Ser Glu Lys Leu Leu Glu Leu Ala Lys 300 305 310			966
ttg gag ttc aac atc ttt cac tcc ctt caa cag aag gag tta cag tat Leu Glu Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr 315 320 325			1014
ctc tcc aga tgg tgg ata cat tcg ggt ttg cct gaa ctg acc ttt ggt Leu Ser Arg Trp Trp Ile His Ser Gly Leu Pro Glu Leu Thr Phe Gly 330 335 340			1062
cgg cat cgt cac gtg gaa tac tac acc ctg agc tct tgc att gcg act Arg His Arg His Val Glu Tyr Tyr Thr Leu Ser Ser Cys Ile Ala Thr 345 350 355			1110
gag ccc aaa cat tct gca ttc aga ttg ggc ttt gcc aaa acg tgt cat Glu Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys Thr Cys His 360 365 370 375			1158
ctt atc acg gtt ctg gac gat atc tac gac act ttc gga acg atg gat Leu Ile Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asp 380 385 390			1206
gaa atc gaa ctc ttc aac gag gca gtt agg aga tgg aat ccg tcg gag Glu Ile Glu Leu Phe Asn Glu Ala Val Arg Arg Trp Asn Pro Ser Glu 395 400 405			1254

aaa gaa cgc ctc cca gaa tat atg aaa gaa atc tac atg gca ctc tac	1302
Lys Glu Arg Leu Pro Glu Tyr Met Lys Glu Ile Tyr Met Ala Leu Tyr	
410 415 420	
gaa gcc tta act gac atg gcg cga gag gca gag aag aca caa ggc cga	1350
Glu Ala Leu Thr Asp Met Ala Arg Glu Ala Glu Lys Thr Gln Gly Arg	
425 430 435	
gac acg ctc aat tat gct aga aag gct tgg gaa gtt tat ctt gat tcg	1398
Asp Thr Leu Asn Tyr Ala Arg Lys Ala Trp Glu Val Tyr Leu Asp Ser	
440 445 450 455	
tat aca caa gaa gca aag tgg atc gcc agc ggt tat ctg cca act ttc	1446
Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe	
460 465 470	
gag gag tac tta gag aac gcg aag gtt agc tct ggt cat cgt gca gcg	1494
Glu Glu Tyr Leu Glu Asn Ala Lys Val Ser Ser Gly His Arg Ala Ala	
475 480 485	
gca ttg aca ccc ctc ctg aca ttg gac gta ccg ctt cct gat gac gtc	1542
Ala Leu Thr Pro Leu Leu Thr Leu Asp Val Pro Leu Pro Asp Asp Val	
490 495 500	
ttg aag gga ata gat ttt cca tcg aga ttt aat gat ttg gca tct tcc	1590
Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser	
505 510 515	
ttc ctt aga cta aga ggt gac aca cga tgc tac aag gca gac agg gac	1638
Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Asp	
520 525 530 535	
cga gga gaa gaa gcg tca agc ata tcg tgt tac atg aaa gac aat ccc	1686
Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro	
540 545 550	
gga tta aca gag gaa gat gct ctc aat cat atc aat gcc atg atc aac	1734
Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn	
555 560 565	
gac ata atc aaa gaa tta aat tgg gaa ctt ctc aaa ccc gat agc aat	1782
Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn	
570 575 580	
att cca atg act gca cgg aaa cat gct tat gag ata acc aga gct ttc	1830
Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe	
585 590 595	
cac caa ctt tac aaa tat aga gat ggc ttc agc gtt gcc act caa gaa	1878
His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu	
600 605 610 615	
acg aaa agt ttg gtg agg aga acg gtc ctt gaa cca gtg cct ctt	1923
Thr Lys Ser Leu Val Arg Arg Thr Val Leu Glu Pro Val Pro Leu	
620 625 630	
taacaattta aaccttctat aataaattgg tgtaggctcc gctatgcgtt tatgcatgtg	1983
catgtctctc tatgtaacta gttgtatgcg tggtatgatt ataaaattgg aggttactcg	2043